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Conference Abstract

Exploring and Reconstructing Ancestral Anatomies using Ontology-Informed Approaches

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Abstract

Ancestral character state reconstruction has been long used to gain insight into the evolution of individual traits in organisms. However, organismal anatomies (= entire phenotypes) are not merely ensembles of individual traits, rather they are complex systems where traits interact with each other due to anatomical dependencies (when one trait depends on the presence of another trait) and developmental constraints. Comparative phylogenetics has been largely lacking a method for reconstructing the evolution of entire organismal anatomies or organismal body regions. Herein, we present a new approach named *PARAMO* (*Phylogenetic Ancestral Reconstruction of Anatomy by Mapping Ontologies, Tarasov and Uyeda 2019*) that takes into account anatomical dependencies and uses stochastic maps (i.e., phylogenetic trees with an instance of mapped evolutionary history of characters, Huelsenbeck et al. 2003) along with anatomy ontologies to reconstruct organismal anatomies.

Our approach treats the entire phenotype or its component body regions as single complex characters and allows exploring and comparing phenotypic evolution at different levels of anatomical hierarchy. These complex characters are constructed by ontology-informed amalgamation of elementary characters (i.e., those coded in character matrix) using stochastic maps. In our approach, characters are linked with the terms from an anatomy

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ontology, which allows viewing them not just as an ensemble of character state tokens but as entities that have their own biological meaning provided by the ontology. This ontology-informed framework provides new opportunities for tracking phenotypic radiations and anatomical evolution of organisms, which we explore using a large dataset for the insect order Hymenoptera (sawflies, wasps, ants and bees).

Keywords

comparative phylogenetics, ontologies, organismal anatomies, trait evolution, Hymenoptera

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